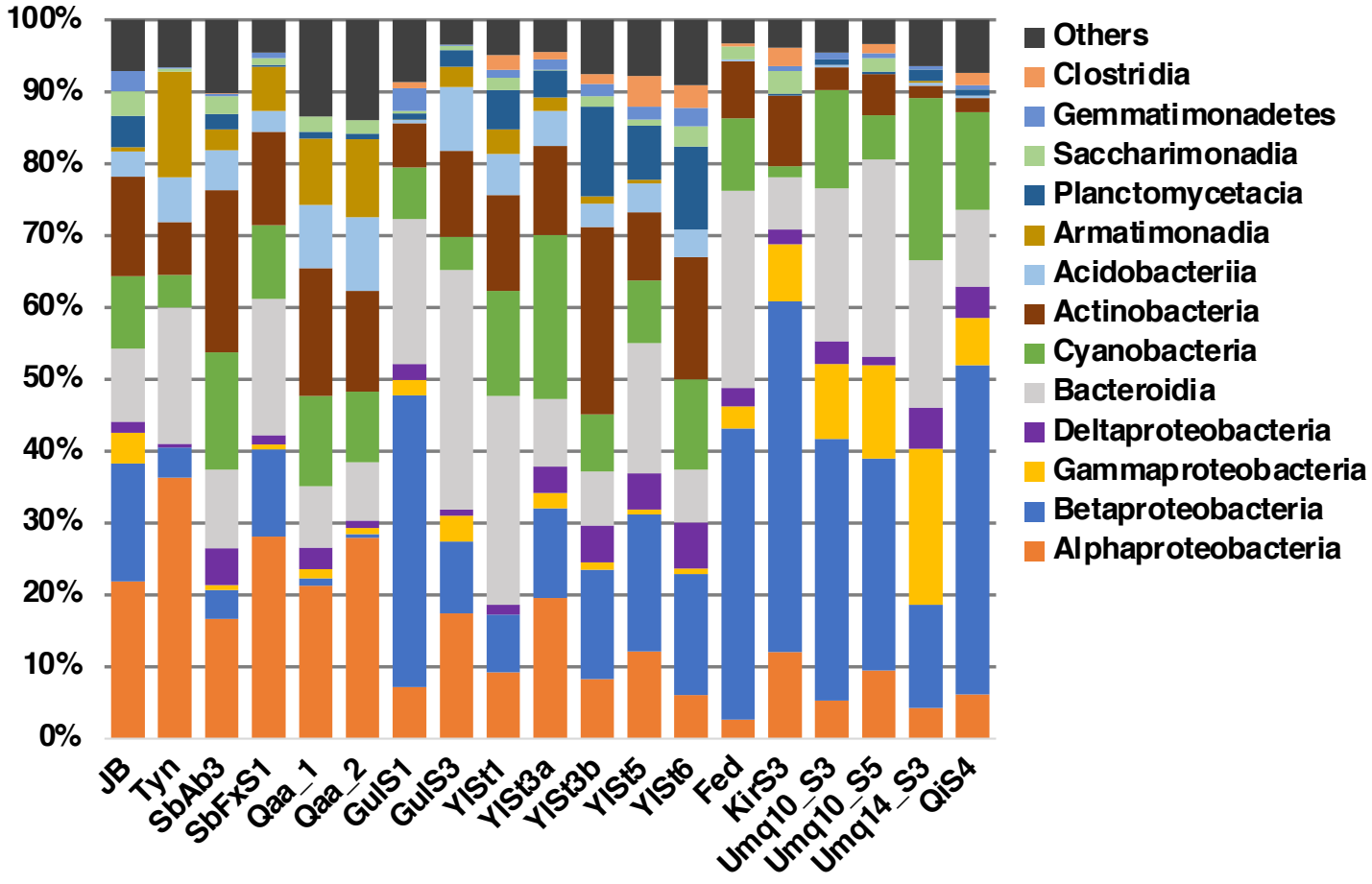
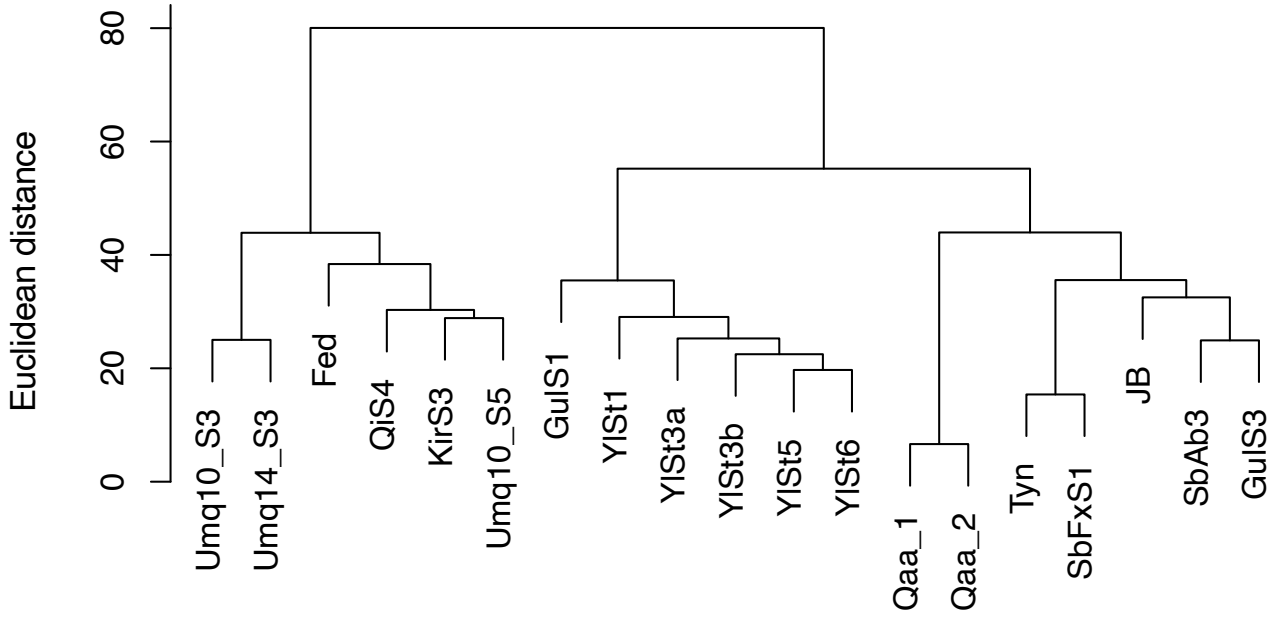



**Figure S1. Bacterial class composition based on 16S rRNA read abundance.**
Taxonomy follows SILVA132 except for Betaproteobacteriales and Oxyphotobaceria; these are indicated as Betaproteobacteria and Cyanobacteria, respectively.

**16S rRNA gene**




**KEGG-annotated gene**

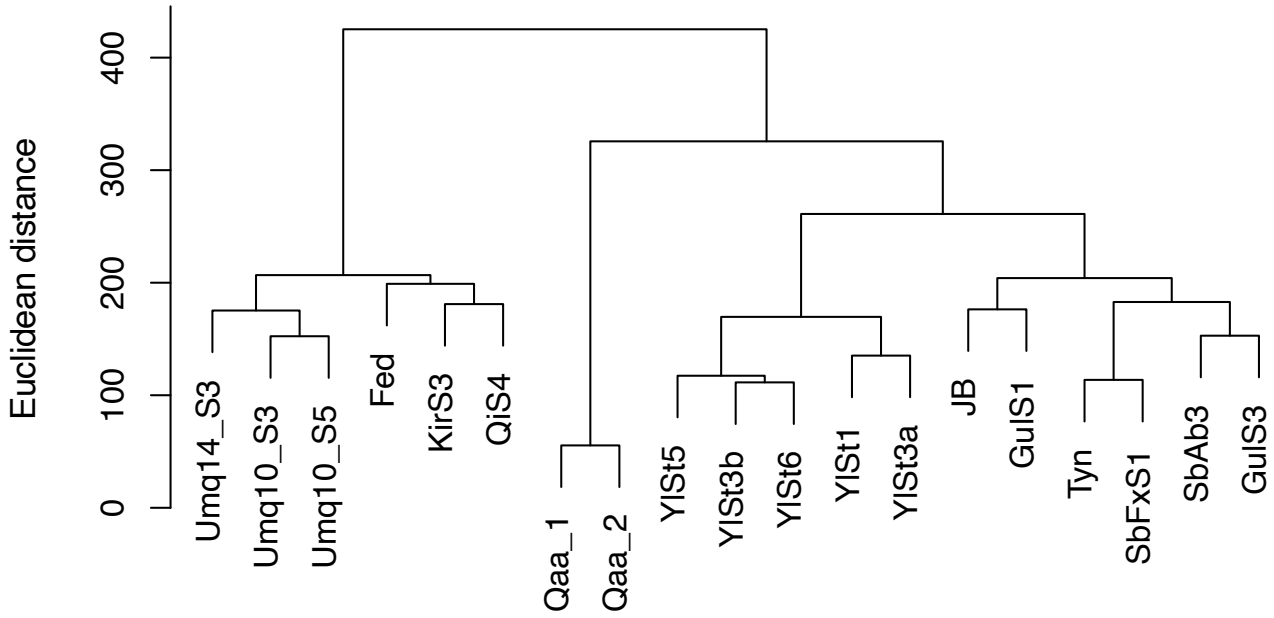



**Figure S2. Hierarchical clustering of cryoconite samples based on the abundance of 16S rRNA genes (upper) and KEGG-annotated genes (lower).**
Pairwise Euclidean distance between the samples was used for clustering with the Ward method. Calculations were carried out by using the *dist* and *hclust* functions in R software.

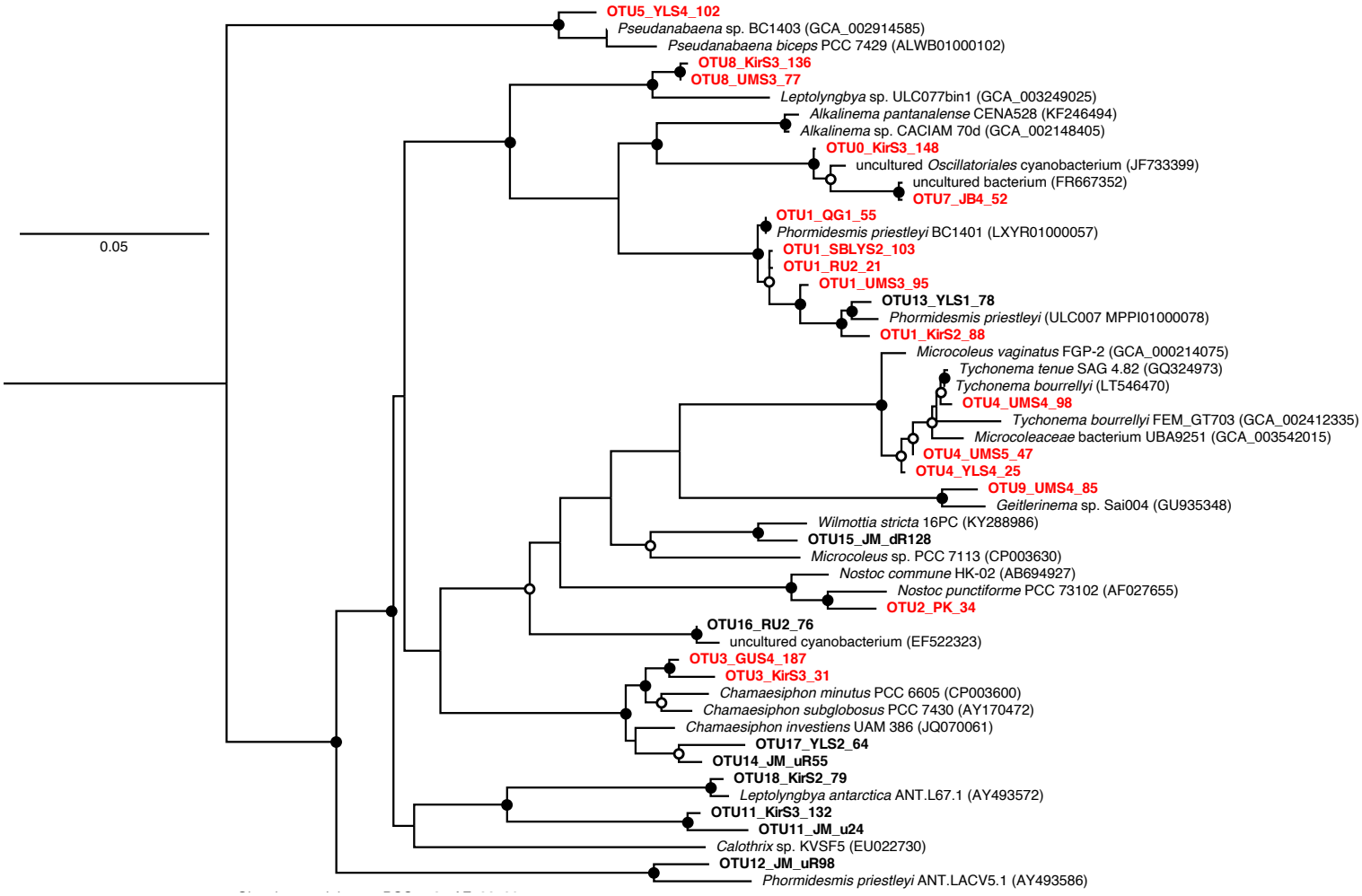



**Figure S3. Phylogenetic positions of 16S rRNA gene phylotypes of *Cyanobacteria*.** Sequences of the operational taxonomic units (OTUs; indicated in bold) were clone-sequenced from the cryoconite samples in Segawa et al. (2017). The OTU groups detected in the present study are shown in red. Bootstrap confidence values ≥50% (open circles) and ≥70% (filled circles) are indicated. *Gloeobacter violaceus* PCC 7421 (AF132790) was used as the outgroup.

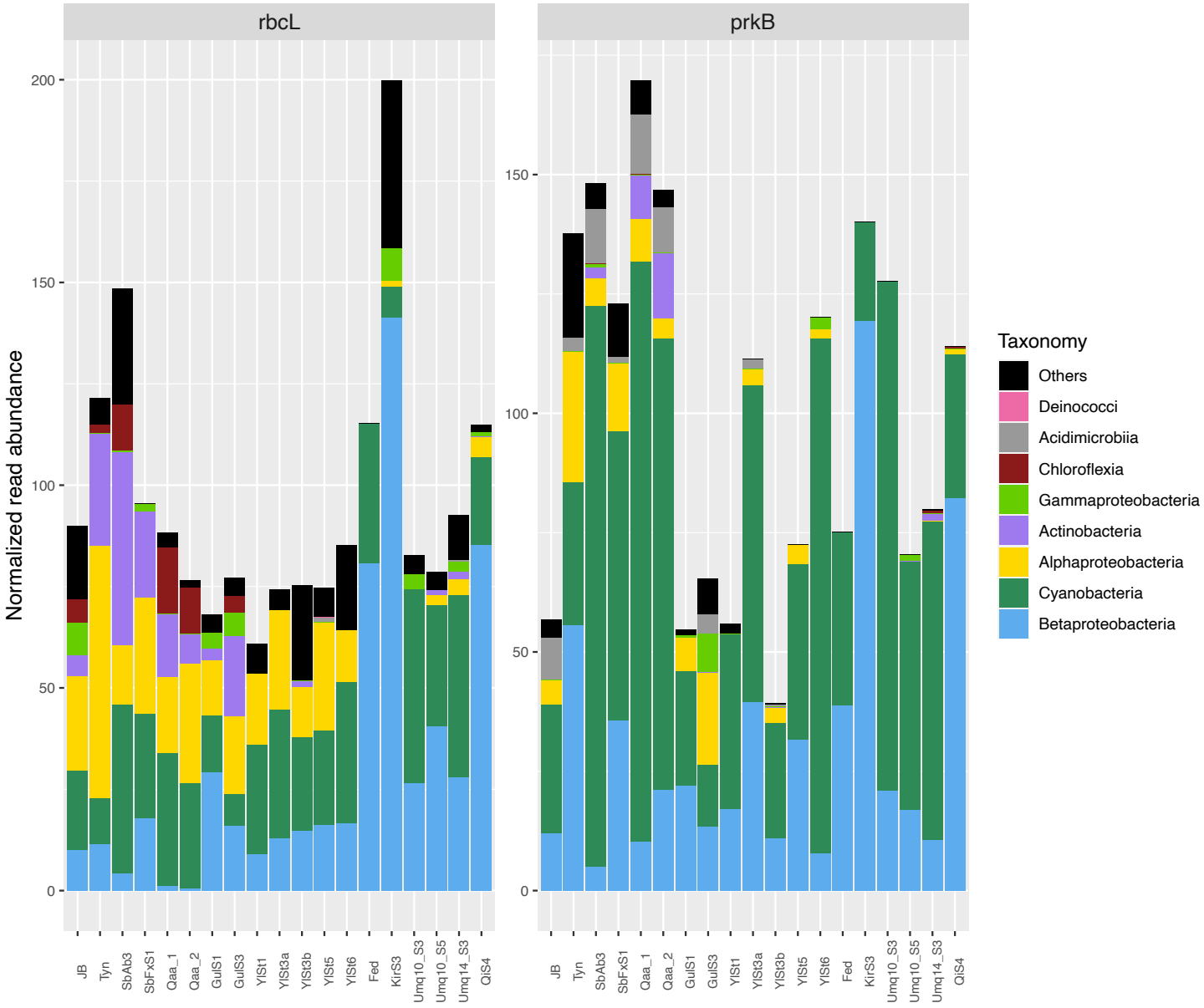



**Figure S4. Read abundance of the genes responsible for $CO_2$ fixation.**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *rbcL*: ribulose-bisphosphate carboxylase large subunit; *prkB*: phosphoribulokinase.

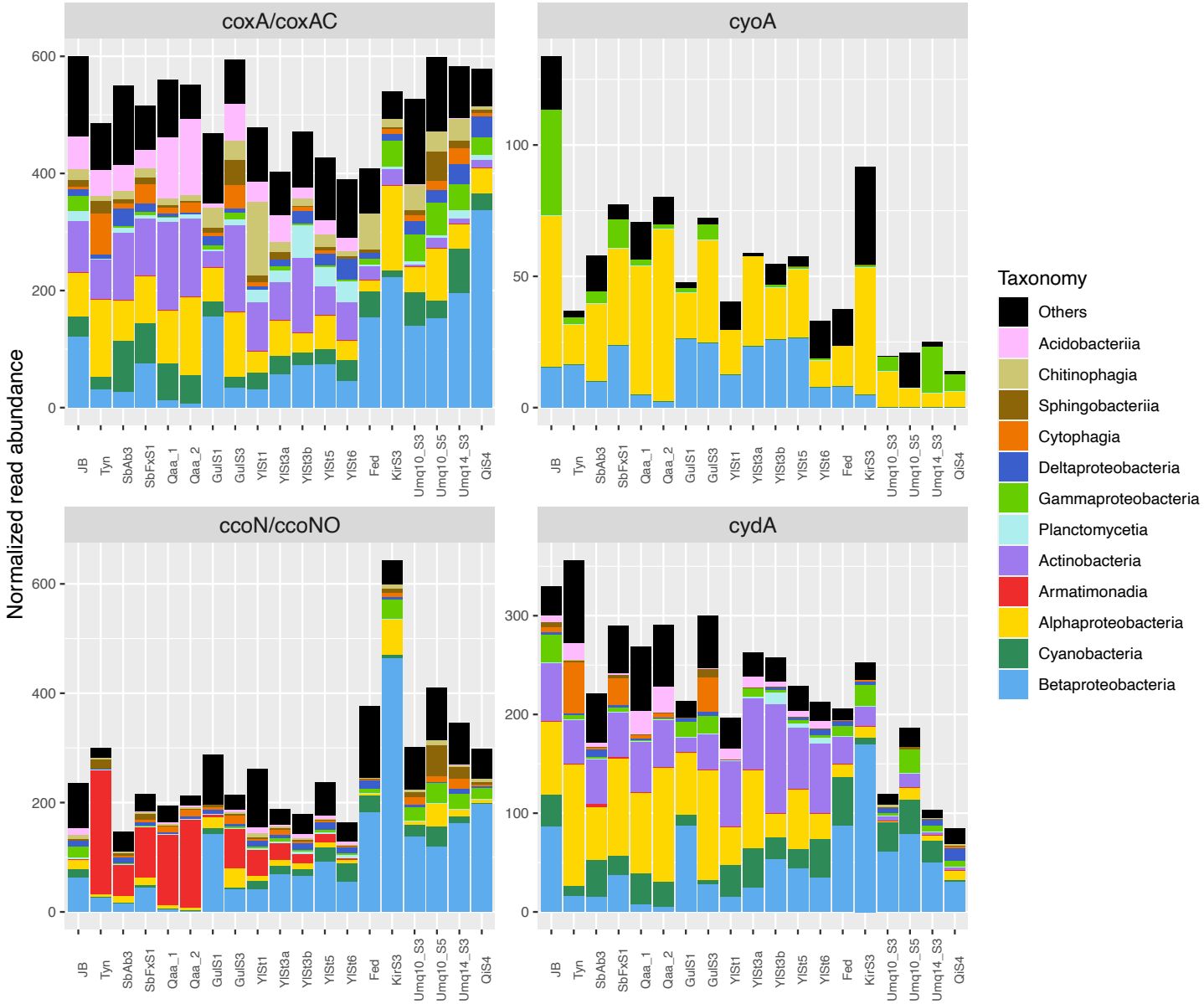



**Figure S5. Read abundance of the genes responsible for aerobic respiration.**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *coxA/coxAC*: cytochrome *c* oxidase subunit I (+ III); *cyoA*: cytochrome *o* ubiquinol oxidase subunit II; *ccoN/ccoNO*: cytochrome *c* oxidase cbb3-type subunit I (+ II) *cydA*: cytochrome *bd* ubiquinol oxidase subunit I.

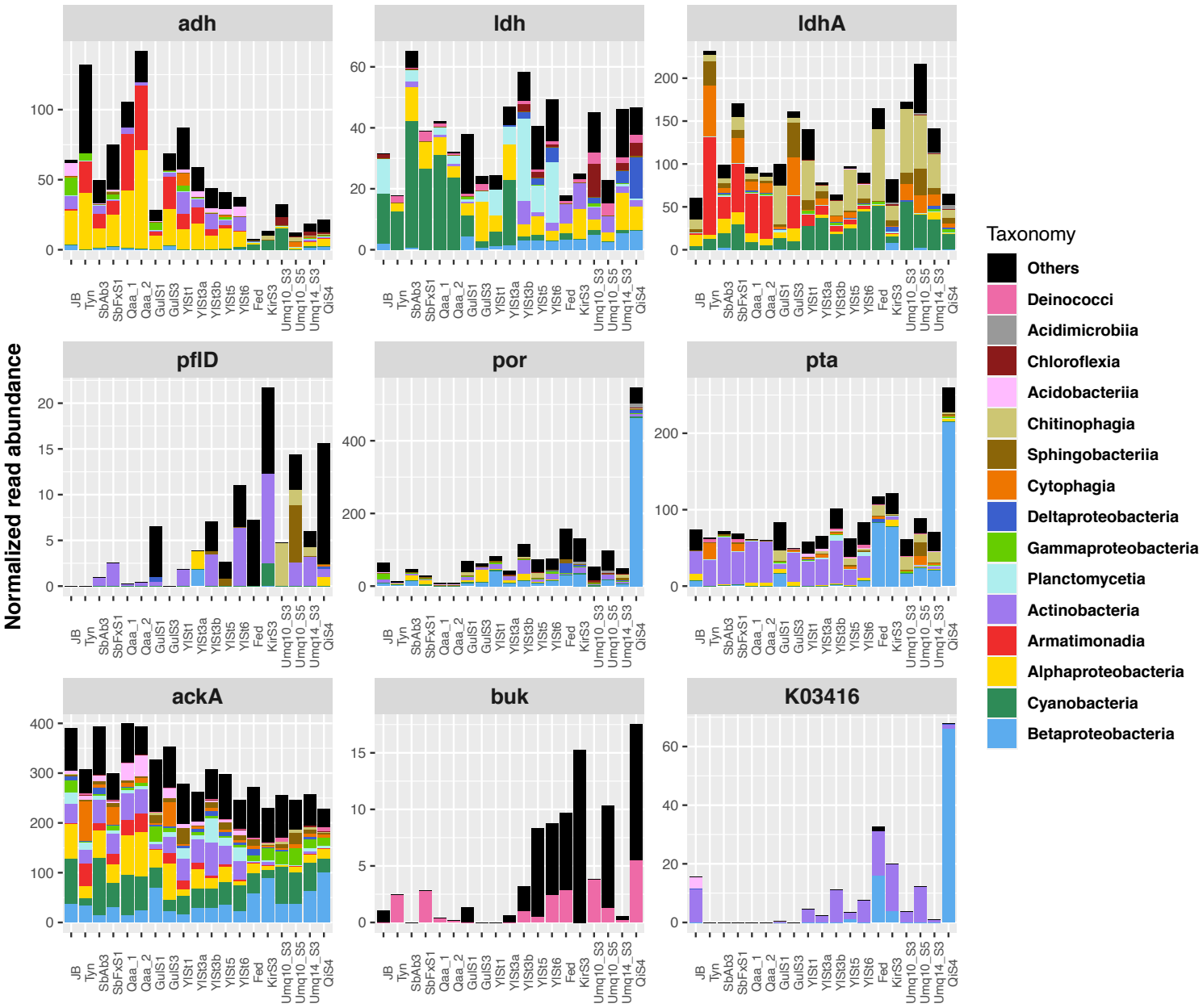



**Figure S6. Read abundance of the genes involved in the fermentation.**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *adh*: alcohol dehydrogenase (KEGG Orthology ID: K00001 and K00002); *ldh*: L-lactate dehydrogenase; *ldhA*: D-lactate dehydrogenase; *plfD*: formate C-acetyltrans -ferase; *por*: pyruvate-ferredoxin oxidoreductase; *pta*: phosphate acetyltransferase; *ackA*: acetate kinase; *buk*: butyrate kinase; K03416: methylmalonyl-CoA carboxyltransferase.

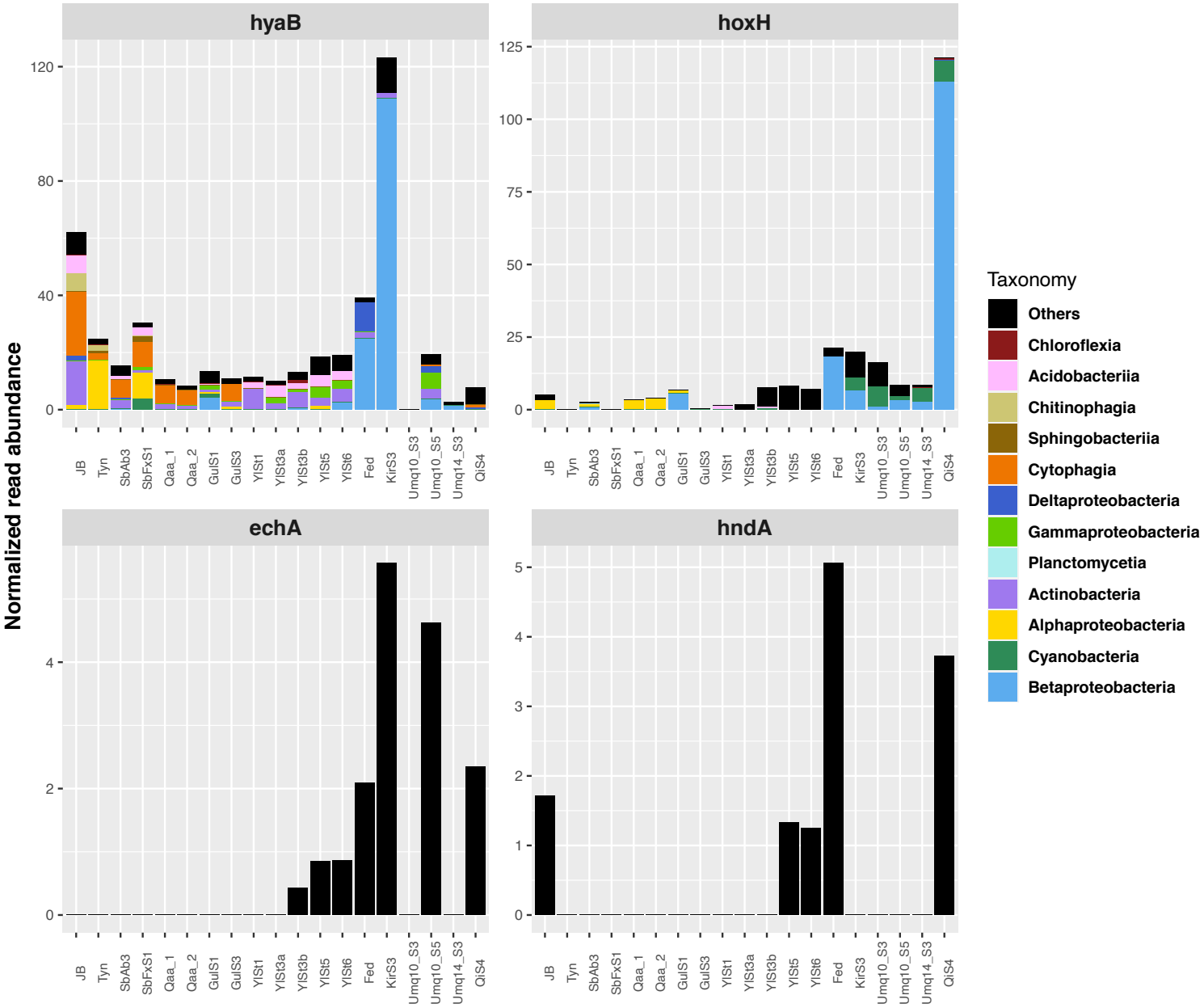



**Figure S7. Read abundance of the genes encoding the subunit of hydrogenases**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *hyaB*: Hya hydrogenase large subunit; *hoxH*: Hox hydrogenase large subunit; *echA*: Ech hydrogenase subunit A; *hndA*: Hnd hydrogenase subunit A.

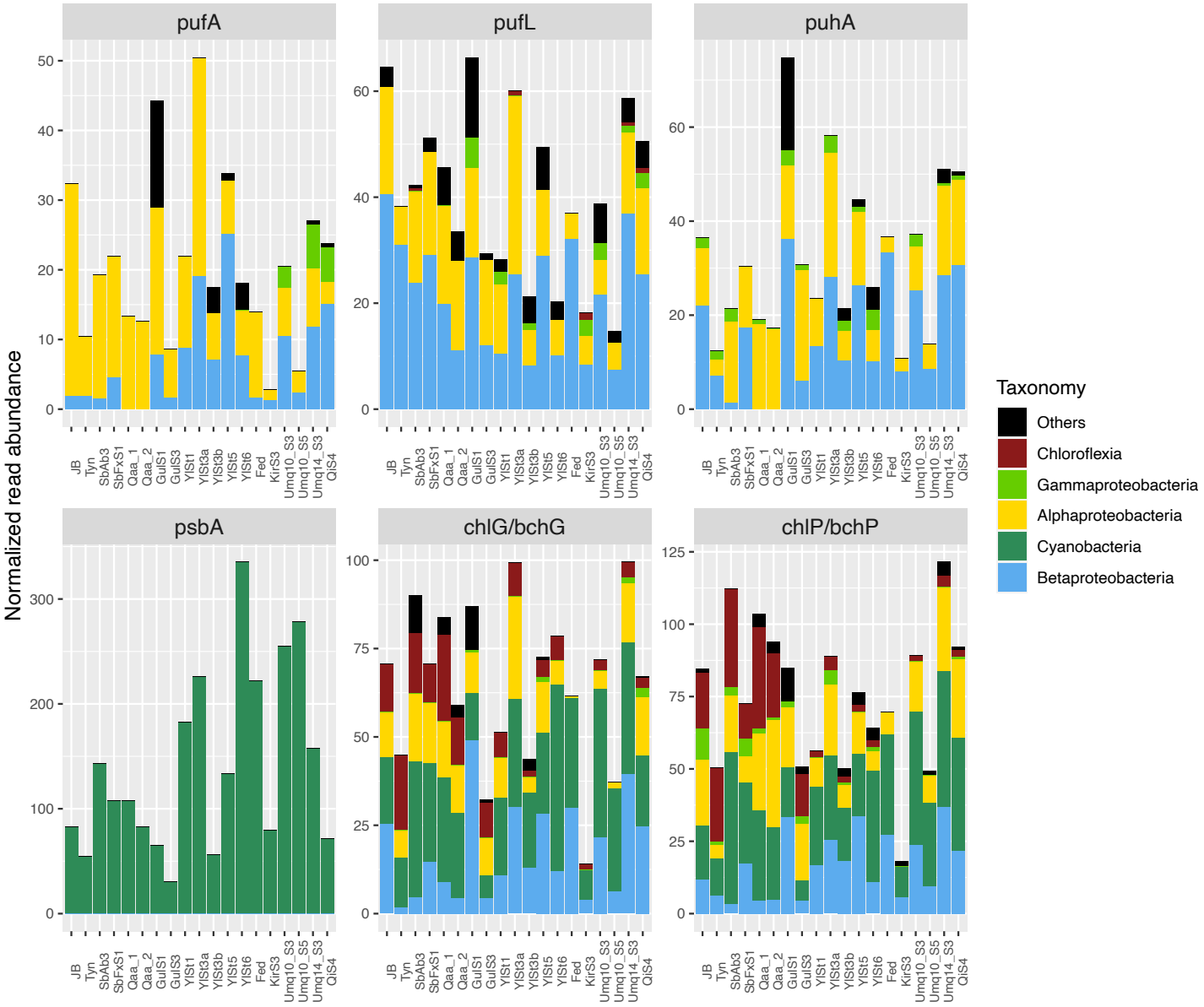



**Figure S8. Read abundance of the genes responsible for photosystems.**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *pufA*: light-harvesting complex 1 alpha chain; *pufL*: photosynthetic reaction center L subunit; *puhA*: photosynthetic reaction center H subunit; *psbA*: photosystem II P680 reaction center D1 protein; *chlG*/*bchG*: chlorophyll/bacteriochlorophyll *a* synthase; *chlP*/*bchP*: geranylgeranyl diphosphate/geranylgeranyl-bacteriochlorophyllide *a* reductase.

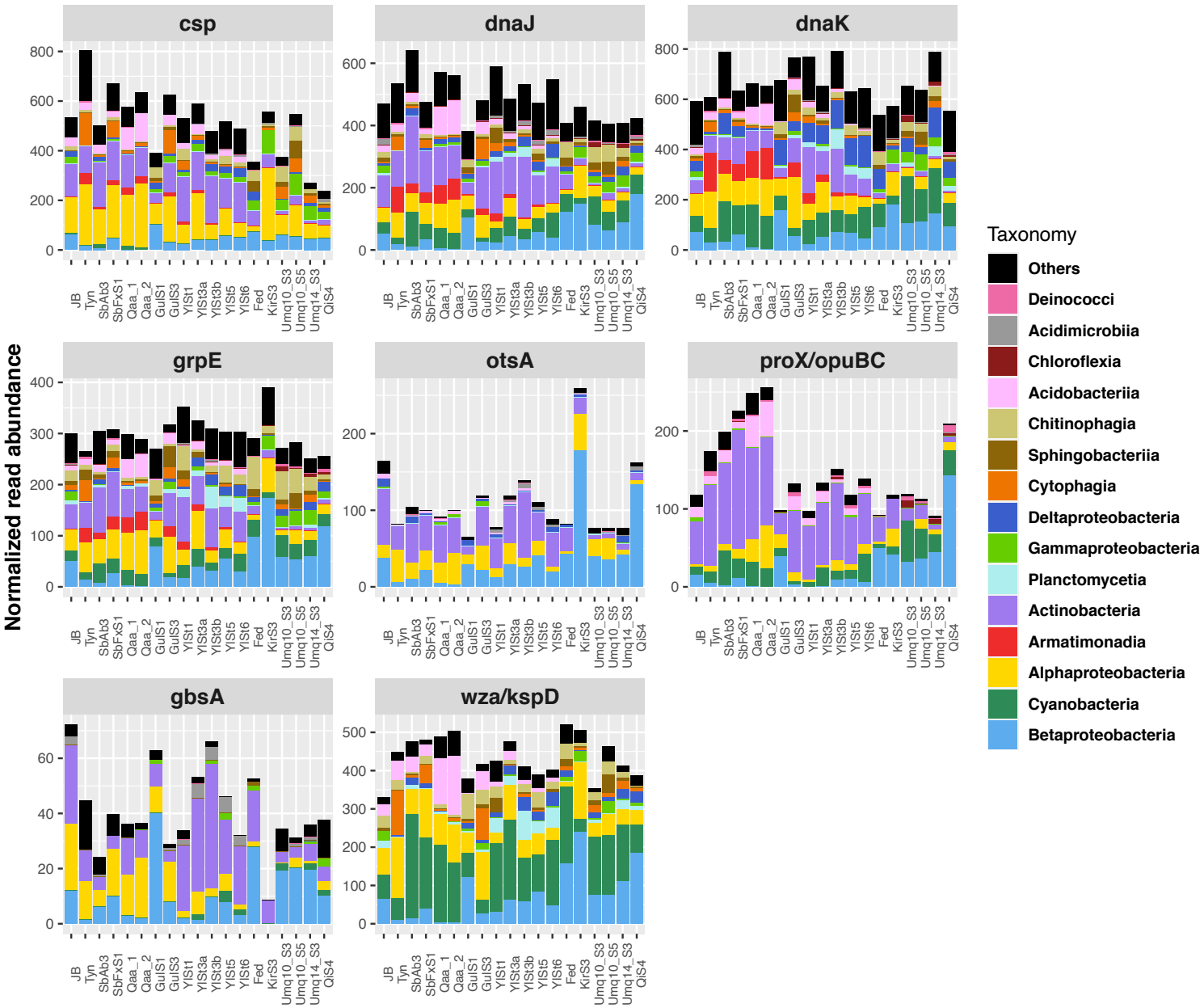



**Figure S9. Read abundance of the genes involved in the psychrotolerance.**
Read abundance was normalized to the total read abundance of KEGG-annotated genes in each sample. *csp*: cold-shock protein family; *dnaJ*: molecular chaperone DnaJ; *dnaK*: molecular chaperone DnaK; *grpE*: molecular chaperone GrpE; *otsA*: trehalose 6-phosphate synthase; *proX/opuBC*: glycine betaine and proline transport system substrate-binding protein; *gbsA*: betaine-aldehyde dehydrogenase; *wza/kspD*: polysaccharide export protein.

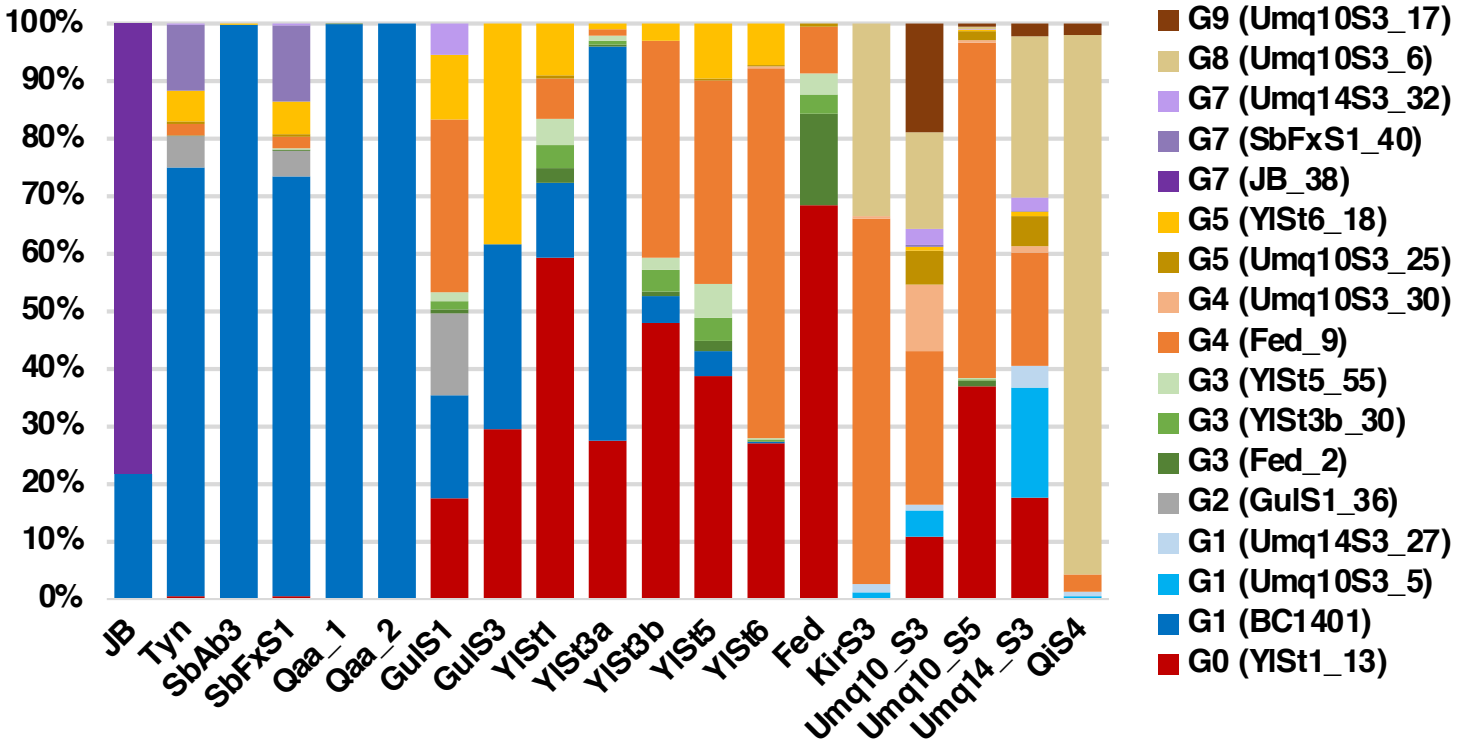



**Figure S10. Composition of cyanobacterial lineages based on the read abundance of the metagenome-assembled genomes (MAGs).**
Sixteen MAGs achieving highest quality scores (Completeness - 2x Contamination) and a draft genome of *Phormidesmis priestleyi* BC1401 were chosen as the references of 17 species-level (ANI ≥95%) cyanobacterial lineages. Composition was calculated based on the median value of read abundance mapped on the protein-coding regions (CDS) within each MAG/draft genome. CDSs which have homologues with ≥98% nucleotide identity were excluded from the calculation.